

SEQUENCE LISTING

<110> IMMUCON INC.
SULLIVAN, Robert
BERUBE, Bruno
LEGARE, Christine
GAUDEFRAULT, Christian

ACROSOMAL SPERM PROTEIN AND USES THEREOF

<130> 13045=2PGT EG/1d

<150> US29/090,567

11518 1938-06-08

<160> 8

<170> FastSEQ for Windows Version 3.0

63107 1

62112 1031

42122 DNA

<213> Artificial Sequence

2202

$\text{O}_2 \text{O}_2 > 0.03$

(222), (124), . . . , (856)

4223> p26h cDNA

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 ttagcagatc aacattdaacc tcagccccctc ccctggccac aggaggacac tggtgtcagc
 agc atg aag ctg aat ttc act ggt ctc agg gct ctg gtg acc ggg gca
 Met Lys Leu Asn Phe Thr Gly Leu Arg Ala Leu Val Thr Gly Ala
 1 5 10 15

ggg aga ggg att ggg cga ggc act gcg aaa gcc ctg cat gcc tca gga 216
 Gly Arg Gly Ile Gly Arg Gly Thr Ala Lys Ala Leu His Ala Ser Gly
 20 25 30

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gcc aaa gtg gtg gcc gtg tca ctc atc aac gaa gac ctg gtc agc ctg 264
Ala Lys Val Val Ala Val Ser Leu Ile Asn Glu Asp Leu Val Ser Leu
          35           40           45

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gcc aaa gag tgt ccg ggc ata gag cct gtg tgt gtg gac ctg ggt gac 312
 Ala Lys Cys Pro Gly Ile Glu Pro Val Cys Val Asp Leu Gly Asp
 50 55 60

... gac gca aca gag aag gca ctg ggc cgt att ggc ccc gtg gac ctg
 Thr Glu Ala Thr Glu Lys Ala Leu Gly Arg Ile Gly Pro Val Asp Leu
 65 70 75

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JAN 30 2003

TECH CENTER 1600/2900

ctg gtg aac aat gcg gcg gtg gcg cta gtg cag cct ttc ata cag tct Leu Val Asn Asn Ala Ala Val Ala Leu Val Gln Pro Phe Ile Gln Ser 80 85 90 95	408
acc aaq qaq qtc ttt qac agg tcc ttc aat gtg aat gtg cgc tat gtg Thr Lys Glu Val Phe Asp Arg Ser Phe Asn Val Asn Arg Ser Val 100 105 110	456
ctg cua gtg tcc cag atg gta gcc aag gyc atg att aac cgt gga gtg Leu Gln Val Ser Gln Met Val Ala Lys Gly Met Ile Asn Arg Gly Val 115 120 125	504
gca gca tcc att gtc aac atc tcc acc atg gtg gcc tat gtc acc ttc Ala Gly Ser Ile Val Asn Ile Ser Ser Met Val Ala Tyr Val Thr Phe 130 135 140	551
cct gyt ctg gcc acc tac agc tcc acc aag ggt gct ata acc atg ctg Pro Gly Leu Ala Thr Tyr Ser Ser Thr Lys Gly Ala Ile Thr Met Leu 145 150 155	600
acc cua gct atg gcc atg gag ctg gga cca tac aag acc tgg gtg aac Thr Lys Ala Met Ala Met Glu Leu Gly Pro Tyr Lys Ile Arg Val Asn 160 165 170 175	648
tct gta aat cct acc gtg gtg act gac atg ggc aag aaa gtc tat Ser Val Asn Pro Thr Val Val Leu Thr Asp Met Gly Lys Lys Val Ser 180 185 190	696
gca gaa ccc gaa tcc gca aag aag ccc aag gag ggc ccc ccc ctg agg Ala Asp Pro Glu Phe Ala Lys Lys Glu Arg His Pro Leu Arg 195 200 .05	744
aag tcc gct gag gtg gag gac gtc aac agc acc ccc ttc ctg ctc Lys Phe Ala Glu Val Glu Asp Val Val Asn Ser Ile Leu Phe Leu Leu 210 215 220	792
agg gag aac aac gcc tct acc agc ggc tat ggc acc cty atg gag gct Ser Asp Ser Ser Ala Ser Thr Ser Gly Ser Gly Ile Leu Val Asp Ala 225 230 235	840
ggc tat ctc gcc tcc t agacggccca ggtgcagggg acttctggag acttccatgg Gly Tyr Leu Ala Ser 240	888
ccccacattt acatcaagac ccgcgcctca acccaaacccaa ataattttgt tccaaatccgt tagagccca ccccacacac atccatcccc aactttagac tccggggatcc cgcattccca taccatgtat gtttgagataa ttgttattaaa taagtatccc aaaccaaaaaaa aaaaaaaaaa aaaaaa	956 1016 10 6 1051
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211 - 244	
212 - PRT	
213 - Artificial Sequence	

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 35 40 45
 Lys Glu Cys Pro Gly Ile Glu Pro Val Cys Val Asp Leu Gly Asp Trp
 50 55 60
 Glu Ala Thr Glu Lys Ala Leu Gly Arg Ile Gly Pro Val Asp Leu Leu
 65 70 75 80
 Val Asn Asn Ala Ala Val Ala Leu Val Gln Pro Phe Ile Gln Ser Thr
 85 90 95
 Lys Glu Val Phe Asp Arg Ser Phe Asn Val Asn Val Arg Ser Val Leu
 100 105 110
 Gln Val Ser Gln Met Val Ala Lys Gly Met Ile Asn Arg Gly Val Ala
 115 120 125
 Gly Ser Ile Val Asn Ile Ser Ser Met Val Ala Tyr Val Thr Phe Pro
 130 135 140
 Gly Leu Aln Thr Tyr Ser Ser Thr Lys Gly Ala Ile Thr Met Leu Thr
 145 150 155 160
 Lys Ala Met Ala Met Glu Leu Gly Pro Tyr Lys Ile Arg Val Asn Ser
 165 170 175
 Val Asn Pro Thr Val Val Leu Thr Asp Met Gly Lys Lys Val Ser Ala
 180 185 190
 Asp Pro Glu Phe Ala Lys Lys Leu Lys Glu Arg His Pro Leu Arg Lys
 195 200 205
 Phe Ala Glu Val Glu Asp Val Val Asn Ser Ile Leu Phe Leu Leu Ser
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 Asp Ser Ser Ala Ser Thr Ser Gly Ser Gly Ile Leu Val Asp Ala Gly
 225 230 235 240
 Tyr Leu Ala Ser

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 <211> 912
 <212> DNA
 <213> Artificial Sequence

<220>
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 accggggcag gcaaaggat agggcgccgc acggtccagg cgctgcacgc gacggggcg 180
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 gggatagaac ccgtgtgcgt ggacctgggt gactgggagg ccaccgagcg ggegctgggs 300
 aacgtggggcc ccgtggaccc gtggtaaac aacgcgcgtg tcgcctgtct gcagcccttc 360
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gttactgagc agacttaggg G

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<211> 19

<212> PRT

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<223> Xaa = Any Amino Acid

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Met Lys Leu Asn Phe Ser Xaa Leu Arg Leu Val Thr Gly Ala Gly Lys

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15

Gly Ile Gly